

Package ‘SurrogateParadoxTest’

September 18, 2024

Type Package

Title Empirical Testing of Surrogate Paradox Assumptions

Version 1.0

Date 2024-09-08

Author Emily Hsiao

Maintainer Emily Hsiao <ehsiao@utexas.edu>

Description Provides functions to nonparametrically assess assumptions necessary to prevent the surrogate paradox through hypothesis tests of stochastic dominance, monotonicity of regression functions, and non-negative residual treatment effects. More details are available in Hsiao et al 2024 (under review).

License GPL

Imports stats, parallel

R topics documented:

test_assumptions 1

Index 4

test_assumptions	<i>Test assumptions to prevent surrogate paradox</i>
------------------	--

Description

Tests the assumptions necessary to prevent the surrogate paradox: stochastic dominance of surrogate values in the treatment group over control group, monotonicity of the relationship between surrogate and primary endpoint in both treatment and control group, and non-negative residual treatment effect of the treatment group over the control group.

Usage

```
test_assumptions(s0 = NULL, y0 = NULL, s1 = NULL, y1 = NULL, trim = 0.95,  
alpha = 0.05, type = "all", all_results = TRUE, direction = "positive",  
parallelize = FALSE, monotonicity_bootstrap_n = 100, nnr_bootstrap_n = 200)
```

Arguments

s0	Vector of surrogate values in control group.
y0	Vector of primary endpoint values in control group.
s1	Vector of surrogate values in treatment group.
y1	Vector of primary endpoint values in treatment group.
trim	Proportion of data to keep after trimming the outliers. Defaults to 95%. Trims data by sorting by surrogate value and removing $(1 - \text{trim})/2$ % of the lowest and highest surrogate values with their corresponding primary endpoint values.
alpha	Desired alpha level of tests.
type	Type of test to run. Defaults to "all"; possible inputs are "sd" (stochastic dominance), "monotonicity" (monotonicity), and "nnr" (non-negative residual treatment effect).
all_results	TRUE or FALSE; return all outputs from hypothesis tests. Defaults to TRUE.
direction	Direction of the test. Defaults to "positive", which tests that the treatment group stochastically dominates the control group, that μ_0 and μ_1 are monotonically increasing, and that $\mu_0 \leq \mu_1 \forall s$. Parameter "negative" tests that the control group stochastically dominates the treatment group, that μ_0 and μ_1 are monotonically decreasing, and that $\mu_1 \leq \mu_0 \forall s$.
parallelize	TRUE or FALSE. Whether to parallelize bootstrap samples of the monotonicity test.
monotonicity_bootstrap_n	Number of bootstrap samples for monotonicity test.
nnr_bootstrap_n	Number of bootstrap samples for nnr test.

Value

result	Table or string of results of the tests
sd_result	Detailed results of stochastic dominance test; only returned if all_results is TRUE
monotonicity0_result	Detailed results of monotonicity test in control group; only returned if all_results is TRUE
monotonicity1_result	Detailed results of monotonicity test in treatment group; only returned if all_results is TRUE
nnr_result	Detailed results of nnr test; only returned if all_results is TRUE

Author(s)

Emily Hsiao

References

- Barrett, Garry F., and Stephen G. Donald. "Consistent tests for stochastic dominance." *Econometrica* 71.1 (2003): 71-104.
- Hall, Peter, and Nancy E. Heckman. "Testing for monotonicity of a regression mean by calibrating for linear functions." *Annals of Statistics* (2000): 20-39.
- Hsiao, Tian, Parast. "Avoiding the Surrogate Paradox: An Empirical Framework for Assessing Assumptions." 2024 (Under Review)

Examples

```
m_c <- function(s) 1 + 2 * s
m_t <- function(s) 1 + 2 * s

s_c <- rnorm(100, 3, 1)
y_c <- sapply(s_c, function(s) rnorm(1, m_c(s), 1))
s_t <- rnorm(100, 3, 1)
y_t <- sapply(s_t, function(s) rnorm(1, m_t(s), 1))

test_assumptions(
  s0 = s_c, y0 = y_c, s1 = s_t, y1 = y_t, type = "sd"
)
```

Index

test_assumptions, [1](#)